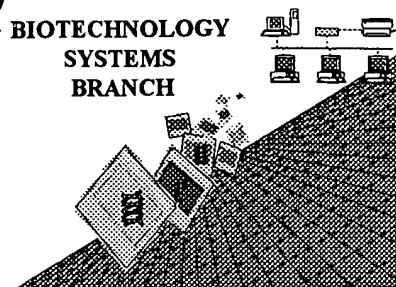


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/305,984

Art Unit / Team No. : 0186

Date Processed by STIC: 5/18/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/305,984

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2:0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/305,984

DATE: 05/18/1999
TIME: 08:42:27

Input Set: I305984.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

*see item 13 on Enr summary sheet for
Hyphenation of these missing
mandatory items*

see item 13

*Does Not Comply
Corrected Diskette Needed*

```

E--> 1 <110>
E--> 2 <120>
W--> 3 <130>
      4 <140> US/09/305,984
      5 <141> 1999-05-05
E--> 6 <160>
      7 <170> PatentIn Ver. 2.0
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      9 <211> 75
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     14      gcaagagact ataat 75
     15 <210> 2
     16 <211> 25
     17 <212> PRT
     18 <213> bacterial
     19 <400> 2
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     21      1 5 10 15
     22      Asp Lys Arg Pro Ala Arg Asp Tyr Asn
     23      20 25
     24 <210> 3
     25 <211> 75
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     27 <213> Artificial Sequence
     28 <220>
     29 <223> Description of Artificial Sequence:primer
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     34 <211> 25
     35 <212> PRT
     36 <213> Artificial Sequence
     37 <220>
     38 <223> Description of Artificial Sequence:primer
     39 <400> 4
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     41      1 5 10 15
     42      Asp Lys Arg Pro Ala Arg Asp Tyr Asn
     43      20 25
     44 <210> 5
  
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RAW SEQUENCE LISTING PATENT APPLICATION US/09/305,984

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46 <212> DNA
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52      gcaagagacg ctaat                                     75
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54 <211> 25
55 <212> PRT
56 <213> Artificial Sequence
57 <220>
58 <223> Description of Artificial Sequence:primer
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61          1             5             10             15
62      Asp Lys Arg Pro Ala Arg Asp Ala Asn
63          20             25
64 <210> 7
65 <211> 42
66 <212> DNA
67 <213> bacterial
68 <400> 7
69      atgagaaagg aatttcacaa cgttttatct agtggtcagt tg                                     42
70 <210> 8
71 <211> 14
72 <212> PRT
73 <213> bacterial
74 <400> 8
75      Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln Leu
76          1             5             10
77 <210> 9
78 <211> 33
79 <212> DNA
80 <213> bacterial
81 <400> 9
82      cttgcagaca aaaggccagc aagagactat aat                                     33
83 <210> 10
84 <211> 11
85 <212> PRT
86 <213> bacterial
87 <400> 10
88      Leu Ala Asp Lys Arg Pro Ala Arg Asp Tyr Asn
89          1             5             10
90 <210> 11
91 <211> 84
92 <212> DNA
93 <213> bacterial
94 <400> 11

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/305,984

DATE: 05/18/1999
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96      aaaaggccag caagagacta taat                                     84
97      <210> 12
98      <211> 28
99      <212> PRT
100     <213> bacterial
101     <400> 12
102     Met Glu Phe Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln
103           1             5             10             15
104     Leu Leu Ala Asp Lys Arg Pro Ala Arg Asp Tyr Asn
105           20             25
106     <210> 13
107     <211> 1329
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113     cgtcaggaaa ccattgggtca aaaggcaaca gccattgccc agtccctaga agggaaagat 180
114     aggcagagta tcgagcaagt gtagacttg tattccaga ctagtatat caaggggacc 240
115     gtcaaagggtg agatgaccga ggacaagtta gaagtcaagg acagtcttcc tctggacaca 300
116     gaccgccaga caacctctct ctttattgag gagcgcgagg tgaaaacgca agacggtggt 360
117     actatgattc tccagtttct agcttccatg gatttacaaa aggaagcgga gcaaatacgt 420
118     ctccagtttc ttccctatac cttgctggcc tcctttctga tttccctttt ggtggcctac 480
119     atctacgctc ggactattgt tgcaccgatt ttggaaatca agcgggtgac ccgtcggatg 540
120     atggacctgg attccaagt gcgattgcgc gtggattcta aggatgagat aggtaatctc 600
121     aaggaacaaa tcaatagcct ctaccagcat ctcttgactg ttattgcgga cttgcatgaa 660
122     aagaatgaag ccattctcca gctggagaag atgaaggctg aattcctacg aggagcttct 720
123     catgaattga aaacaccgct ggctagtttg aaaatcctaa tcgaaaatat gagagagaat 780
124     atcggtcggt ataaggatag agaccagtat ctgggagttg ccttggggat tgtggatgaa 840
125     ctcaatcacc atgttctgca gatactttcc ctctcttctg tgcaggaatt gcgagatgat 900
126     agggaaacaa ttgacctcct ccagatgacg caaaatctgg tcaaagatta tgcttgcta 960
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129     ccagggtggct tagttcgaat tggagaaaga gaaggagaac tttttatcga aaatagctgt 1140
130     agctcagagg aacaagaaaa actagcccag tctttttctg acaatgccag tcgcaagggtc 1200
131     aaggggtctg gtatggggct ctttgtggtt aagagtctat tagaacatga aaaattagct 1260
132     tatcgtttct agatggagga gaatagttta accttcttta tagattttcc aaaagtcgtc 1320
133     caagactag                                     1329
134     <210> 14
135     <211> 442
136     <212> PRT
137     <213> bacterial
138     <400> 14
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140           1             5             10             15
141     Ile Phe Ser Val Leu Val Ile Cys Leu His Leu Ala Ile Tyr Phe Leu
142           20             25             30
143     Phe Pro Ser Thr Tyr Leu Ser His Arg Gln Glu Thr Ile Gly Gln Lys
144           35             40             45

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RAW SEQUENCE LISTING
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```

145   Ala Thr Ala Ile Ala Gln Ser Leu Glu Gly Lys Asp Arg Gln Ser Ile
146           50                      55                      60
147   Glu Gln Val Leu Asp Leu Tyr Ser Gln Thr Ser Asp Ile Lys Gly Thr
148       65                      70                      75                      80
149   Val Lys Gly Glu Met Thr Glu Asp Lys Leu Glu Val Lys Asp Ser Leu
150           85                      90                      95
151   Pro Leu Asp Thr Asp Arg Gln Thr Thr Ser Leu Phe Ile Glu Glu Arg
152           100                     105                     110
153   Glu Val Lys Thr Gln Asp Gly Gly Thr Met Ile Leu Gln Phe Leu Ala
154           115                     120                     125
155   Ser Met Asp Leu Gln Lys Glu Ala Glu Gln Ile Ser Leu Gln Phe Leu
156           130                     135                     140
157   Pro Tyr Thr Leu Leu Ala Ser Phe Leu Ile Ser Leu Leu Val Ala Tyr
158   145                      150                      155                      160
159   Ile Tyr Ala Arg Thr Ile Val Ala Pro Ile Leu Glu Ile Lys Arg Val
160           165                      170                      175
161   Thr Arg Arg Met Met Asp Leu Asp Ser Gln Val Arg Leu Arg Val Asp
162           180                      185                      190
163   Ser Lys Asp Glu Ile Gly Asn Leu Lys Glu Gln Ile Asn Ser Leu Tyr
164           195                      200                      205
165   Gln His Leu Leu Thr Val Ile Ala Asp Leu His Glu Lys Asn Glu Ala
166           210                      215                      220
167   Ile Leu Gln Leu Glu Lys Met Lys Val Glu Phe Leu Arg Gly Ala Ser
168   225                      230                      235                      240
169   His Glu Leu Lys Thr Pro Leu Ala Ser Leu Lys Ile Leu Ile Glu Asn
170           245                      250                      255
171   Met Arg Glu Asn Ile Gly Arg Tyr Lys Asp Arg Asp Gln Tyr Leu Gly
172           260                      265                      270
173   Val Ala Leu Gly Ile Val Asp Glu Leu Asn His His Val Leu Gln Ile
174           275                      280                      285
175   Leu Ser Leu Ser Ser Val Gln Glu Leu Arg Asp Asp Arg Glu Thr Ile
176           290                      295                      300
177   Asp Leu Leu Gln Met Thr Gln Asn Leu Val Lys Asp Tyr Ala Leu Leu
178   305                      310                      315                      320
179   Ala Lys Glu Arg Glu Leu Gln Ile Asp Asn Ser Leu Thr His Gln Gln
180           325                      330                      335
181   Ala Tyr Leu Asn Pro Ser Val Met Lys Leu Ile Leu Ser Asn Leu Ile
182           340                      345                      350
183   Ser Asn Ala Ile Lys His Ser Val Pro Gly Gly Leu Val Arg Ile Gly
184           355                      360                      365
185   Glu Arg Glu Gly Glu Leu Phe Ile Glu Asn Ser Cys Ser Ser Glu Glu
186           370                      375                      380
187   Gln Glu Lys Leu Ala Gln Ser Phe Ser Asp Asn Ala Ser Arg Lys Val
188   385                      390                      395                      400
189   Lys Gly Ser Gly Met Gly Leu Phe Val Val Lys Ser Leu Leu Glu His
190           405                      410                      415
191   Glu Lys Leu Ala Tyr Arg Phe Glu Met Glu Glu Asn Ser Leu Thr Phe
192           420                      425                      430
193   Phe Ile Asp Phe Pro Lys Val Val Gln Asp
194           435                      440

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/305,984

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195 <210> 15
196 <211> 657
197 <212> DNA
198 <213> bacterial
199 <400> 15
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202 tctagctatg aggtggccct ggttttactg gatattccaga tgcccaagct caacggctta 180
203 gaagtcctag ctgagattcg taaaaccagt caggttcctg tcttgatggt gacagctttt 240
204 caagatgagg aatacaagat gagtgccttt gcctctttgg cagatggcta tctggaaaaa 300
205 cctttctccc tctccctttt aaaagtgagg gtggacgcga ttttcaagcg ctactacgat 360
206 acaggacgaa tcttttctta caaggatacc aagggtggact ttgaaagcta cagtgcgaagc 420
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208 aaaaatgaag gccgggcctt gactcgatct cagattatcg atgccgtctg gaaagcgaca 540
209 gatgagggtt cctttgaccg tgttattgat gtttatatca aggaattgcg gaaaaagcta 600
210 gacttggatt gtatcctcac tgtgcgcaat gttggttata aattggagcg aaaatga 657

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION US/09/305,984DATE: 05/18/1999
TIME: 08:42:27

Input Set: I305984.RAW

Line	? Error/Warning	Original Text
1	E Response to "Applicant" Name is Missing	
2	E Response to "Title of Invention" Missing	
3	W Response to "File Reference" is Missing	
6	E # of Seq. 0 Not Equal Actual 54	
809	W "N" or "Xaa" used: Feature required	Asp Lys Arg Pro Ala Arg Asp Xaa Asn
834	W "N" or "Xaa" used: Feature required	Arg Lys Glu Phe His Xaa Xaa Xaa Xaa Xaa X
836	W "N" or "Xaa" used: Feature required	Lys Arg Pro Xaa Arg Asp Tyr
872	W "N" or "Xaa" used: Feature required	Met Xaa Xaa Xaa Xaa Xaa Asn Val Leu Ser X
874	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Asn